

(1) GENERAL INFORMATION:

(1) GENERAL INFORMATION:

- GENERAL INFORMATION:
- (i) APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
 - (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
 - (iii) NUMBER OF SEQUENCES: 75
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/486,050
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/127,499
 - (B) FILING DATE: 28-SEP-1993
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENT, Stephen A.
 - (B) REGISTRATION NUMBER: 29,768
 - (C) REFERENCE/DOCKET NUMBER: 51916/103/INBI
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 672-5300
 - (B) TELEFAX: (202) 672-5399
 - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 992 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Thr Pro Ile Thr Met Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Ser	Thr	Thr	Pro	Ile	Thr	Met	Glu	Asp	Leu	Gln	Lys	Ala	Leu
1				5					10					15	
	Glu	Ala	Gln	Ser	Arg	Ala	Leu	Arg	Ala	Gly	Leu	Ala	Ala	Gly	Ala
				20				25						30	Ser

Gln Ser Arg Arg Pro Arg Pro Pro Arg His Ala Arg Leu Gln His Leu
35 40 45

Pro Glu Met Thr Pro Ala Val Thr Pro Glu Gly Pro Ala Pro Pro Arg
50 55 60

Thr Gly Ala Trp Gln Arg Lys Asp Trp Ser Arg Ala Pro Pro Pro Pro
65 70 75 80

Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser
85 90 95

Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly Arg
100 105 110

Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro Phe
115 120 125

Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro Asp
130 135 140

Thr Glu Ala Pro Thr Glu Ala Cys Val Thr Ser Trp Leu Trp Ser Glu
145 150 155 160

Gly Glu Gly Ala Val Phe Tyr Arg Val Asp Leu His Phe Ile Asn Leu
165 170 175

Gly Thr Pro Pro Leu Asp Glu Asp Gly Arg Trp Asp Pro Ala Leu Met
180 185 190

Tyr Asn Pro Cys Gly Pro Glu Pro Pro Ala His Val Val Arg Ala Tyr
195 200 205

Asn Gln Pro Ala Gly Asp Val Arg Gly Val Trp Gly Lys Gly Glu Arg
210 215 220

Thr Tyr Ala Glu Gln Asp Phe Arg Val Gly Gly Thr Arg Trp His Arg
225 230 235 240

Leu Leu Arg Met Pro Val Arg Gly Leu Asp Gly Asp Thr Ala Pro Leu
245 250 255

Pro Pro His Thr Thr Glu Arg Ile Glu Thr Arg Ser Ala Arg His Pro
260 265 270

Trp Arg Ile Arg Phe Gly Ala Pro Gln Ala Phe Leu Ala Gly Leu Leu
275 280 285

Leu Ala Ala Val Ala Val Gly Thr Ala Arg Ala Gly Leu Gln Pro Arg
290 295 300

Ala Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His
305 310 315 320

Gly Gln His Tyr Gly His His His His Gln Leu Pro Phe Leu Gly His
325 330 335

Asp Gly His His Gly Gly Thr Leu Arg Val Gly Gln His His Arg Asn
340 345 350

Ala Ser Asp Val Leu Pro Gly His Trp Leu Gln Gly Gly Trp Gly Cys
355 360 365

Tyr Asn Leu Ser Asp Trp His Gln Gly Thr His Val Cys His Thr Lys
370 375 380

His Met Asp Phe Trp Cys Val Glu His Asp Arg Pro Pro Pro Ala Thr
385 390 395 400

Pro Thr Ser Leu Thr Thr Ala Ala Asn Tyr Ile Ala Ala Ala Thr Pro
405 410 415

Ala Thr Ala Pro Pro Pro Cys His Ala Gly Leu Asn Asp Ser Cys Gly
420 425 430

Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Pro Thr Ala Leu Thr
435 440 445

Pro Gly Ala Val Gly Asp Leu Arg Ala Val His His Arg Pro Val Pro
450 455 460

Ala Tyr Pro Val Cys Cys Ala Met Arg Trp Gly Leu Pro Pro Trp Glu
465 470 475 480

Leu Val Ile Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys Arg Gly
485 490 495

Val Pro Ala His Pro Gly Thr Arg Cys Pro Glu Leu Val Ser Pro Met
500 505 510

Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala Thr Ala
515 520 525

Asn Ala Leu Ser Leu Asp His Ala Phe Ala Ala Phe Val Leu Leu Val
530 535 540

Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg Arg Pro
545 550 555 560

Ala Pro Pro Pro Pro Ser Pro Gln Ser Ser Cys Arg Gly Thr Thr Pro
565 570 575

Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala Pro Gly
580 585 590

Cys Ala Thr Gln Thr Pro Val Pro Val Arg Leu Ala Gly Val Gly Phe
595 600 605

Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp Leu Glu
610 615 620

Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser Cys Glu
625 630 635 640

Gly Leu Gly Ala Trp Val Pro Thr Ala Pro Cys Ala Arg Ile Trp Asn
645 650 655

Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr Ser Ser
660 665 670

Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly Ser Tyr
675 680 685

Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala Phe Gly
690 695 700

His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val Met Ser
705 710 715 720

Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr Val Arg
725 730 735

9

81
-4

Val	Lys	Phe	His	Thr	Glu	Thr	Arg	Thr	Val	Trp	Gln	Leu	Ser	Val	Ala	
			740					745					750			
Gly	Val	Ser	Cys	Asn	Val	Thr	Thr	Glu	His	Pro	Phe	Cys	Asn	Thr	Pro	
		755					760					765				
His	Gly	Gln	Leu	Glu	Val	Gln	Val	Pro	Pro	Asp	Pro	Gly	Asp	Leu	Val	
	770					775					780					
Glu	Tyr	Ile	Met	Asn	Tyr	Thr	Gly	Asn	Gln	Gln	Ser	Arg	Trp	Gly	Leu	
785					790					795					800	
Gly	Ser	Pro	Asn	Cys	His	Gly	Pro	Asp	Trp	Ala	Ser	Pro	Val	Cys	Gln	
			805					810						815		
Arg	His	Ser	Pro	Asp	Cys	Ser	Arg	Leu	Val	Gly	Ala	Thr	Pro	Glu	Arg	
			820					825					830			
Pro	Arg	Leu	Arg	Leu	Val	Asp	Ala	Asp	Asp	Pro	Leu	Leu	Arg	Thr	Ala	
		835					840					845				
Pro	Gly	Pro	Gly	Glu	Val	Trp	Val	Thr	Pro	Val	Ile	Gly	Ser	Gln	Ala	
	850					855					860					
Arg	Lys	Cys	Gly	Leu	His	Ile	Arg	Ala	Gly	Pro	Tyr	Gly	His	Ala	Thr	
865					870					875					880	
Val	Glu	Met	Pro	Glu	Trp	Ile	His	Ala	His	Thr	Thr	Ser	Asp	Pro	Trp	
				885					890					895		
His	Pro	Pro	Gly	Pro	Leu	Gly	Leu	Lys	Phe	Lys	Thr	Val	Arg	Pro	Val	
			900					905					910			
Ala	Leu	Pro	Arg	Ala	Leu	Ala	Pro	Pro	Arg	Asn	Val	Arg	Val	Thr	Gly	
		915					920					925				
Cys	Tyr	Gln	Cys	Gly	Thr	Pro	Ala	Leu	Val	Glu	Gly	Leu	Ala	Pro	Gly	
	930					935					940					
Gly	Gly	Asn	Cys	His	Leu	Thr	Val	Asn	Gly	Glu	Asp	Val	Gly	Ala	Phe	
945					950					955					960	
Pro	Pro	Gly	Lys	Phe	Val	Thr	Ala	Ala	Leu	Leu	Asn	Thr	Pro	Pro	Pro	
			965						970				975			
Tyr	Gln	Val	Ser	Cys	Gly	Gly	Glu	Ser	Asp	Arg	Ala	Ser	Ala	Gly	His	
			980					985					990			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro	Ser	Arg	Ala	Pro	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Arg	Met	Gln	Thr
1				5				10						15	

9

82
-5-

Gly Arg Gly Gly Ser
20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Pro Gln Pro Pro Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg
1 5 10 15
Ala Pro Pro Gln Gln
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Thr Pro Ala Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly
1 5 10 15
Gln His Tyr Gly His
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Pro Gln Pro Pro Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1063 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
1 5 10 15
Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser
20 25 30
Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser
35 40 45
Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Arg Gly
50 55 60
Asn Arg Gly Arg Gly Gln Arg Arg Asp Trp Ser Arg Ala Pro Pro Pro
65 70 75 80
Pro Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro
85 90 95
Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly
100 105 110
Arg Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro
115 120 125
Phe Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro
130 135 140

Asp Thr Glu Ala Pro Thr Glu Ala Cys Val Thr Ser Trp Leu Trp Ser
 145 150 155 160
 Glu Gly Gln Gly Ala Val Phe Tyr Arg Val Asp Leu His Phe Thr Asn
 165 170 175
 Leu Gly Thr Pro Pro Leu Asp Glu Asp Gly Arg Trp Asp Pro Ala Leu
 180 185 190
 Met Tyr Asn Pro Cys Gly Pro Glu Pro Pro Ala His Val Val Arg Ala
 195 200 205
 Tyr Asn Gln Pro Ala Gly Asp Val Arg Gly Val Trp Gly Lys Gly Glu
 210 215 220
 Arg Thr Tyr Ala Glu Gln Asp Phe Arg Val Gly Gly Thr Arg Trp His
 225 230 235 240
 Arg Leu Leu Arg Met Pro Val Arg Gly Leu Asp Gly Asp Ser Ala Pro
 245 250 255
 Leu Pro Pro His Thr Thr Glu Arg Ile Glu Thr Arg Ser Ala Arg His
 260 265 270
 Pro Trp Arg Ile Arg Phe Gly Ala Pro Gln Ala Phe Leu Ala Gly Leu
 275 280 285
 Leu Leu Ala Thr Val Ala Val Gly Thr Ala Arg Ala Gly Leu Gln Pro
 290 295 300
 Arg Ala Asp Met Ala Ala Pro Pro Thr Leu Pro Gln Pro Pro Cys Ala
 305 310 315 320
 His Gly Gln His Tyr Gly His His His His Gln Leu Pro Phe Leu Gly
 325 330 335
 His Asp Gly His His Gly Gly Thr Leu Arg Val Gly Gln His Tyr Arg
 340 345 350
 Asn Ala Ser Asp Val Leu Pro Gly His Trp Leu Gln Gly Gly Trp Gly
 355 360 365
 Cys Tyr Asn Leu Ser Asp Trp His Gln Gly Thr His Val Cys His Thr
 370 375 380
 Lys His Met Asp Phe Trp Cys Val Glu His Ala Arg Pro Pro Pro Ala
 385 390 395 400
 Thr Pro Thr Pro Leu Thr Thr Ala Ala Asn Ser Thr Thr Ala Ala Thr
 405 410 415
 Pro Ala Thr Ala Pro Ala Pro Cys His Ala Gly Leu Asn Asp Ser Cys
 420 425 430
 Gly Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Arg His Gly Ala
 435 440 445
 Asp Thr Arg Cys Gly Arg Leu Ile Cys Gly Leu Ser Thr Thr Ala Gln
 450 455 460
 Tyr Pro Pro Thr Arg Phe Gly Cys Ala Met Arg Trp Gly Leu Pro Pro
 465 470 475 480
 Trp Glu Leu Val Val Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys
 485 490 495

Arg Gly Val Pro Ala His Pro Gly Ala Arg Cys Pro Glu Leu Val Ser
500 505 510

Pro Met Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala
515 520 525

Thr Ala Asn Ala Leu Ser Leu Asp His Ala Leu Ala Ala Phe Val Leu
530 535 540

Ser Val Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg
545 550 555 560

Arg Arg Gly Ala Ala Ala Ala Leu Thr Ala Val Val Leu Gln Gly Tyr
565 570 575

Asn Pro Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala
580 585 590

Pro Gly Cys Ala Thr Gln Ala Pro Val Pro Val Arg Leu Ala Gly Val
595 600 605

Arg Phe Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp
610 615 620

Leu Glu Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser
625 630 635 640

Cys Glu Gly Leu Gly Ala Trp Val Pro Ala Ala Pro Cys Ala Arg Ile
645 650 655

Trp Asn Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr
660 665 670

Ser Ser Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly
675 680 685

Ser Tyr Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala
690 695 700

Phe Gly His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val
705 710 715 720

Met Ser Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr
725 730 735

Val Arg Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser
740 745 750

Val Ala Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn
755 760 765

Thr Pro His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp
770 775 780

Leu Val Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp
785 790 795 800

Gly Leu Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val
805 810 815

Cys Gln Arg His Ser Pro Asp Cys Ser Arg Leu Val Gly Ala Thr Pro
820 825 830

Glu Arg Pro Arg Leu Arg Leu Val Asp Ala Asp Asp Pro Leu Leu Arg
835 840 845

9

86
-8-

Thr Ala Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val Ile Gly Ser
850 855 860

Gln Ala Arg Lys Cys Gly Leu His Ile Arg Ala Gly Pro Tyr Gly His
865 870 875 880

Ala Thr Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp
885 890 895

Pro Trp His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg
900 905 910

Pro Val Ala Leu Pro Arg Thr Leu Ala Pro Pro Arg Asn Val Arg Val
915 920 925

Thr Gly Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala
930 935 940

Pro Gly Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly
945 950 955 960

Ala Val Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro
965 970 975

Pro Pro Tyr Gln Val Ser Cys Gly Gly Glu Ser Asp Arg Ala Ser Ala
980 985 990

Arg Val Ile Asp Pro Ala Ala Gln Ser Phe Thr Gly Val Val Tyr Gly
995 1000 1005

Thr His Thr Thr Ala Val Ser Glu Thr Arg Gln Thr Trp Ala Glu Trp
1010 1015 1020

Ala Ala Ala His Trp Trp Gln Leu Thr Leu Gly Ala Thr Cys Ala Leu
1025 1030 1035 1040

Pro Leu Ala Gly Leu Leu Ala Cys Cys Ala Lys Cys Leu Tyr Tyr Leu
1045 1050 1055

Arg Gly Ala Ile Ala Pro Arg
1060

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Met Ala Ala Pro Pro Thr Leu Pro Gln Pro Pro Arg Ala His Gly
1 5 10 15

Gln His Tyr Gly His
20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid

9

87

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Pro Gln Pro Pro Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225 230 235 240
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
245 250 255
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
260 265 270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
275 280 285
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290 295 300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305 310 315 320
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
325 330 335
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
340 345 350
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
355 360 365
Gln Val Thr Asn Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
370 375 380
Asn Gln Arg Lys Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385 390 395 400
Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
405 410 415
Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
420 425 430
Phe Leu Gly Lys Ile Cys Leu Pro Thr Arg Glu Gly Gln Gly Ile Phe
435 440 445
Phe Arg Ala Asp Gln Ser Gln Gln Pro His His Phe Phe Arg Ala Asp
450 455 460
Gln Ser Gln Gln Pro His Gln Lys Arg Ala Ser Gly Leu Gly
465 470 475

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn
1 5 10 15
Ala Trp Val Lys Val
20

9

89
-12-

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Ala Ile Ser Pro Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15
Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45
Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80
Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110
Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125
Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140
Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160
Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr
275 280 285

Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg
305 310 315 320

Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys
325 330 335

Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser
340 345 350

Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln
355 360 365

Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly
370 375 380

Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp
385 390 395 400

Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser
405 410 415

Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp
420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile
435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
450 455 460

Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
500 505 510

Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val
530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
595 600 605

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
675 680 685

Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
690 695 700

Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
705 710 715 720

Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
725 730 735

Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
740 745 750

Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
755 760 765

Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
770 775 780

Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
785 790 795 800

Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
805 810 815

Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
820 825 830

Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
850 855 860

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
1 5 10 15
Glu Leu Leu Glu Leu
20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Asn Gln Gln Glu Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Lys Thr Thr Leu Lys Met Thr Ala Leu Ala Ala Leu Ser Ala Phe
1 5 10 15
Val Leu Ala Gly Cys Gly Ser His Gln Met Lys Ser Glu Glu His Ala
20 25 30
Asn Met Gln Leu Gln Gln Gln Ala Val Leu Gly Leu Asn Trp Met Gln
35 40 45
Asp Ser Gly Glu Tyr Lys Ala Leu Ala Tyr Gln Ala Tyr Asn Ala Ala
50 55 60
Lys Val Ala Phe Asp His Ala Lys Val Ala Lys Gly Lys Lys Lys Ala
65 70 75 80
Val Val Ala Asp Leu Asp Glu Thr Met Leu Asp Asn Ser Pro Tyr Ala
85 90 95
Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp Thr
100 105 110
Arg Trp Val Asp Ala Arg Gln Ser Arg Ala Val Pro Gly Ala Val Glu
115 120 125

Phe Asn Asn Tyr Val Asn Ser His Asn Gly Lys Val Phe Tyr Val Thr
130 135 140

Asn Arg Lys Asp Ser Thr Glu Lys Ser Gly Thr Ile Asp Asp Met Lys
145 150 155 160

Arg Leu Gly Phe Asn Gly Val Glu Glu Ser Ala Phe Tyr Leu Lys Lys
165 170 175

Asp Lys Ser Ala Lys Ala Ala Arg Phe Ala Glu Ile Glu Lys Gln Gly
180 185 190

Tyr Glu Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly Asn
195 200 205

Thr Val Tyr Gly Lys Leu Asn Ala Asp Arg Arg Ala Phe Val Asp Gln
210 215 220

Asn Gln Gly Lys Phe Gly Lys Thr Phe Ile Met Leu Pro Asn Ala Asn
225 230 235 240

Tyr Gly Gly Trp Glu Gly Gly Leu Ala Glu Gly Tyr Phe Lys Lys Asp
245 250 255

Thr Gln Gly Gln Ile Lys Ala Arg Leu Asp Ala Val Gln Ala Trp Asp
260 265 270

Gly Lys

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Ser Pro Tyr Ala Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp
1 5 10 15

Gly Lys Asp Trp Thr
20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Asn Asn Lys Pro
1 5

9

94
17

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile	Gln	Pro	Pro	Lys	Asn	Leu	Leu	Phe	Ser	Ser	Leu	Leu	Phe	Ser	Ser	1	5	10	15
Leu	Leu	Phe	Ser	Ser	Ala	Ala	Gln	Ala	Ala	Ser	Glu	Asp	Arg	Arg	Ser	20	25	30	
Pro	Tyr	Tyr	Val	Gln	Ala	Asp	Leu	Ala	Tyr	Ala	Ala	Glu	Arg	Ile	Thr	35	40	45	
His	Asp	Tyr	Pro	Gln	Ala	Thr	Gly	Ala	Asn	Asn	Thr	Ser	Thr	Val	Ser	50	55	60	
Asp	Tyr	Phe	Arg	Asn	Ile	Arg	Ala	His	Ser	Ile	His	Pro	Arg	Val	Ser	65	70	75	80
Val	Gly	Tyr	Asp	Phe	Gly	Gly	Trp	Arg	Ile	Ala	Ala	Asp	Tyr	Ala	Ser	85	90	95	
Tyr	Arg	Lys	Trp	Asn	Asn	Asn	Lys	Tyr	Ser	Val	Asn	Thr	Lys	Glu	Leu	100	105	110	
Glu	Asn	Lys	His	Asn	Asn	Lys	Lys	Asp	Leu	Lys	Thr	Glu	Asn	Gln	Glu	115	120	125	
Asn	Gly	Thr	Phe	His	Ala	Ala	Ser	Ser	Leu	Gly	Leu	Ser	Ala	Ile	Tyr	130	135	140	
Asp	Phe	Lys	Leu	Lys	Gly	Lys	Phe	Lys	Pro	Tyr	Ile	Gly	Ala	Arg	Val	145	150	155	160
Ala	Tyr	Gly	His	Val	Arg	His	Ser	Ile	Asp	165	170								

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile	Gln	Pro	Pro	Lys	Asn	Leu	Leu	Phe	Ser	Ser	Leu	Leu	1	5	10
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Gln Pro Pro Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Leu Met Ile Xaa Lys Phe Val Thr Lys Met Xaa Tyr Lys Thr Leu
1 5 10 15

Asp Lys Tyr Leu Arg Arg Arg Leu Ile Leu Asn Ile Ser Ile Val Xaa
20 25 30

Lys Xaa Leu Ser Glu Lys Arg Xaa Ile Xaa Met Asn Lys Lys Lys Met
35 40 45

Ile Leu Thr Ser Leu Ala Ser Val Ala Ile Leu Gly Ala Gly Phe Val
50 55 60

Ala Ser Gln Pro Thr Val Val Arg Ala Glu Glu Ser Pro Val Ala Ser
65 70 75 80

Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala Ala Lys Lys Asp Ala Lys
85 90 95

Asn Ala Lys Lys Ala Val Glu Asp Ala Gln Lys Ala Leu Asp Asp Ala
100 105 110

Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp Gln Lys Lys Thr Glu Glu
115 120 125

Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu Glu Met Asp Lys Ala Val
130 135 140

Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr Gln Gln Ala Thr Asp Lys
145 150 155 160

Ala Ala Lys Asp Ala Ala Asp Lys Met Ile Asp Glu Ala Lys Lys Arg
165 170 175

Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr Val Arg Ala Met Val Val
180 185 190

Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys Lys Lys Ser Glu Glu Ala
195 200 205

Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys Leu Glu Glu Ala Lys Ala
210 215 220

Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln Lys Val
225 230 235 240

Asp Ala Glu Glu Val Ala Pro Gln Ala Lys Ile Ala Glu Leu Glu Asn
245 250 255

Gln Val His Arg Leu Glu Gln Glu Leu Lys Glu Ile Asp Glu Ser Glu
260 265 270

Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg Ala Pro Leu Gln Ser Lys
275 280 285

Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys Leu Glu Glu Leu Ser Asp
290 295 300

Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala Lys Leu Glu Asp Gln Leu
305 310 315 320

Lys Ala Ala Glu Glu Asn Asn Asn Val Glu Asp Tyr Phe Lys Glu Gly
325 330 335

Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala Glu Leu Glu Lys Thr Glu
340 345 350

Ala Asp Leu Lys Lys Ala Val Asn Glu Pro Glu Lys Pro Ala Pro Ala
355 360 365

Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala Glu Gln Pro Lys Pro Ala
370 375 380

Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys Pro Glu Lys Pro Ala Glu
385 390 395 400

Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln Gln Ala Glu Glu Asp Tyr
405 410 415

Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu Thr Gln Gln Gln Pro
420 425 430

Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Thr Gly Trp Lys Gln
435 440 445

Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Thr
450 455 460

Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ser Asn Gly
465 470 475 480

Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu
485 490 495

Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser
500 505 510

Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln
515 520 525

Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr
530 535 540

Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
545 550 555 560

Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu
565 570 575

Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser
580 585 590

Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Val Lys
595 600 605

Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala
610 615 620

Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu
625 630 635 640

Gly Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala
645 650 655

Asn Gly Glu Trp Val Xaa Ala Asp Xaa Ile Lys Ala Cys Xaa Glu His
660 665 670

Leu Thr Phe Xaa Phe Xaa Asn Lys Asp Lys Val Arg Leu Asn Arg Phe
675 680 685

Met Phe Val Phe Phe Arg Tyr
690 695

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Glu Tyr Asn Arg Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys
1 5 10 15

Pro Ala Pro Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Gln Gln Pro Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

a

98
-21

(A) LENGTH: 484 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Asn	Met	Lys	Lys	Ala	Thr	Ile	Ala	Ala	Thr	Ala	Gly	Ile	Ala	Val	
1			5					10					15			
Thr	Ala	Phe	Arg	Ala	Pro	Thr	Ile	Arg	Ser	Ala	Ser	Thr	Val	Val	Val	
			20					25					30			
Glu	Ala	Gly	Asp	Thr	Leu	Trp	Gly	Ile	Ala	Gln	Ser	Lys	Gly	Thr	Thr	
		35					40					45				
Val	Asp	Ala	Ile	Lys	Lys	Ala	Asn	Asn	Leu	Thr	Thr	Asp	Lys	Ile	Val	
	50					55					60					
Pro	Gly	Gln	Lys	Leu	Gln	Val	Asn	Asn	Glu	Val	Ala	Ala	Ala	Glu	Lys	
65				70					75					80		
Thr	Glu	Lys	Ser	Val	Ser	Ala	Thr	Trp	Leu	Asn	Val	Arg	Ser	Gly	Ala	
			85					90						95		
Gly	Val	Asp	Asn	Ser	Ile	Ile	Thr	Ser	Ile	Lys	Gly	Gly	Thr	Lys	Val	
			100					105					110			
Thr	Val	Glu	Thr	Thr	Glu	Ser	Asn	Gly	Trp	His	Lys	Ile	Thr	Tyr	Asn	
		115					120					125				
Asp	Gly	Lys	Thr	Gly	Phe	Val	Asn	Gly	Lys	Tyr	Leu	Thr	Asp	Lys	Ala	
	130					135					140					
Val	Ser	Thr	Pro	Val	Ala	Pro	Thr	Gln	Glu	Val	Lys	Lys	Glu	Thr	Thr	
145				150					155					160		
Thr	Gln	Gln	Ala	Ala	Pro	Ala	Ala	Glu	Thr	Lys	Thr	Glu	Val	Lys	Gln	
			165					170					175			
Thr	Thr	Gln	Ala	Thr	Thr	Pro	Ala	Pro	Lys	Val	Ala	Glu	Thr	Lys	Glu	
		180					185					190				
Thr	Pro	Val	Val	Asp	Gln	Asn	Ala	Thr	Thr	His	Ala	Val	Lys	Ser	Gly	
		195				200					205					
Asp	Thr	Ile	Trp	Ala	Leu	Ser	Val	Lys	Tyr	Gly	Val	Ser	Val	Gln	Asp	
	210					215					220					
Ile	Met	Ser	Trp	Asn	Asn	Leu	Ser	Ser	Ser	Ser	Ile	Tyr	Val	Gly	Gln	
225				230					235					240		
Lys	Leu	Ala	Ile	Lys	Gln	Thr	Ala	Asn	Thr	Ala	Thr	Pro	Lys	Ala	Glu	
			245					250					255			
Val	Lys	Thr	Glu	Ala	Pro	Ala	Ala	Glu	Lys	Gln	Ala	Ala	Pro	Val	Val	
		260					265					270				
Lys	Glu	Asn	Thr	Asn	Thr	Asn	Thr	Ala	Thr	Thr	Glu	Lys	Lys	Glu	Thr	
		275				280						285				
Ala	Thr	Gln	Gln	Gln	Thr	Ala	Pro	Lys	Ala	Pro	Thr	Glu	Ala	Ala	Lys	
	290					295					300					

Pro Ala Pro Ala Pro Ser Thr Asn Thr Asn Ala Asn Lys Thr Asn Thr
305 310 315 320
Asn Thr Asn Thr Asn Thr Asn Thr Asn Asn Thr Asn Thr Asn Thr Pro
325 330 335
Ser Lys Asn Thr Asn Thr Asn Ser Asn Thr Asn Thr Asn Thr Asn Ser
340 345 350
Asn Thr Asn Ala Asn Gln Gly Ser Ser Asn Asn Asn Ser Asn Ser Ser
355 360 365
Ala Ser Ala Ile Ile Ala Glu Ala Gln Lys His Leu Gly Lys Ala Tyr
370 375 380
Ser Trp Gly Gly Asn Gly Pro Thr Thr Phe Asp Cys Ser Gly Tyr Thr
385 390 395 400
Lys Tyr Val Phe Ala Lys Ala Gly Ile Ser Leu Pro Arg Thr Ser Gly
405 410 415
Ala Gln Tyr Ala Ser Thr Thr Arg Ile Ser Glu Ser Gln Ala Lys Pro
420 425 430
Gly Asp Leu Val Phe Phe Asp Tyr Gly Ser Gly Ile Ser His Val Gly
435 440 445
Ile Tyr Val Gly Asn Gly Gln Met Ile Asn Ala Gln Asp Asn Gly Val
450 455 460
Lys Tyr Asp Asn Ile His Gly Ser Gly Trp Gly Lys Tyr Leu Val Gly
465 470 475 480
Phe Gly Arg Val

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Val Ser Thr Pro Val Ala Pro Thr Gln Glu Val Lys Lys Glu Thr
1 5 10 15
Thr Thr Gln Gln Ala
20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Pro Thr Gln Glu Val Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Lys Gln Thr Thr Gln Ala Thr Thr Pro Ala Pro Lys Val Ala Glu
1 5 10 15
Thr Lys Glu Thr Pro
20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Thr Pro Ala Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Ala Ile Lys Gln Thr Ala Asn Thr Ala Thr Pro Lys Ala Glu Val
1 5 10 15
Lys Thr Glu Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Thr Ala Thr Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Lys Glu Thr Ala Thr Gln Gln Gln Thr Ala Pro Lys Ala Pro Thr
1 5 10 15

Glu Ala Ala Lys Pro
20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Gln Thr Ala Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
1 5 10 15

102
25

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
20 25 30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
35 40 45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
50 55 60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
65 70 75 80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
85 90 95
Pro Lys Thr

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Thr Gln Thr Pro Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys
1 5 10 15
Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg
20 25 30
Glu Ala Val Ile Phe Lys Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
35 40 45
Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
50 55 60
Pro Lys Leu
65

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Gln Thr Pro Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Gln Gln Gln Pro Ala Ala
1 5

9

104
-275

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Thr Ile Pro Ile Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gln Ala Gln Thr Asn Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Tyr Thr Thr Val Pro Lys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Thr Gly Thr Ser Lys Ser
1 5

Q

105
-28

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Gln Gln Thr Ala Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gln Thr Gln Phe Ser Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Thr Gln Gly Pro Tyr Ser
1 5

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Pro Pro Gln Thr Pro Pro Thr
1 5

9

104
-29-

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gln Ala Gln Pro Asn Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gln Thr Gln Pro Ser Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Ser Gln Thr Pro Leu Asn
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Glu Thr Ser Val Pro Lys Cys
1 5

9

107
-30-

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gln Thr Arg Asp Thr Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Val Ser Thr Gln Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Trp Thr Lys Asp Pro Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Asn Gln Lys Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gln Ser Leu Thr Thr Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gln Thr Gln Thr Asp Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Leu Gln Asp Gly Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Glu Gly Pro Lys Ile
1 5

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asn Thr Asn Thr Ser Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Thr Ala Ala Pro Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gln Gly Glu Thr His Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gln Gln Pro Ala Pro Ala Thr
1 5

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Thr Gln Ser Ala Lys Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gln Thr Thr Thr Pro Thr Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gln Thr Gln Thr Pro Val Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gln Pro Ala Ser Ser Lys Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Pro Asp Thr Pro Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Val Thr His Pro Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ile Gln Pro Pro Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Gln Pro Pro Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Thr Gln Val Ala Ala Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala
 1 5 10 15
 Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg
 20 25 30
 Gln Gln Gln Pro Pro Lys Ala
 35

His 385	Met	Asp	Phe	Trp	Cys 390	Val	Glu	His	Asp	Arg 395	Pro	Pro	Pro	Ala	Thr 400
Pro	Thr	Ser	Leu	Thr 405	Thr	Ala	Ala	Asn	Tyr 410	Ile	Ala	Ala	Ala	Thr 415	Pro
Ala	Thr	Ala	Pro 420	Pro	Pro	Cys	His	Ala 425	Gly	Leu	Asn	Asp	Ser	Cys	Gly
Gly	Phe	Leu	Ser 435	Gly	Cys	Gly	Pro	Met	Arg	Leu	Pro	Thr 445	Ala	Leu	Thr
Pro	Gly 450	Ala	Val	Gly	Asp	Leu	Arg	Ala	Val	His	His 460	Arg	Pro	Val	Pro
Ala	Tyr	Pro	Val	Cys	Cys 470	Ala	Met	Arg	Trp	Gly 475	Leu	Pro	Pro	Trp	Glu 480
Leu	Val	Ile	Leu	Thr 485	Ala	Arg	Pro	Glu	Asp 490	Gly	Trp	Thr	Cys	Arg 495	Gly
Val	Pro	Ala	His 500	Pro	Gly	Thr	Arg	Cys 505	Pro	Glu	Leu	Val	Ser 510	Pro	Met
Gly	Arg	Ala 515	Thr	Cys	Ser	Pro	Ala 520	Ser	Ala	Leu	Trp	Leu 525	Ala	Thr	Ala
Asn 530	Ala	Leu	Ser	Leu	Asp	His 535	Ala	Phe	Ala	Ala	Phe 540	Val	Leu	Leu	Val
Pro 545	Trp	Val	Leu	Ile	Phe 550	Met	Val	Cys	Arg	Arg 555	Ala	Cys	Arg	Arg	Pro 560
Ala	Pro	Pro	Pro	Pro	Ser 565	Pro	Gln	Ser	Ser 570	Cys	Arg	Gly	Thr	Thr 575	Pro
Pro	Ala	Tyr	Gly 580	Glu	Glu	Ala	Phe	Thr 585	Tyr	Leu	Cys	Thr 590	Ala	Pro	Gly
Cys	Ala	Thr 595	Gln	Thr	Pro	Val	Pro	Val	Arg	Leu	Ala	Gly 605	Val	Gly	Phe
Glu 610	Ser	Lys	Ile	Val	Asp	Gly 615	Gly	Cys	Phe	Ala	Pro 620	Trp	Asp	Leu	Glu
Ala 625	Thr	Gly	Ala	Cys	Ile 630	Cys	Glu	Ile	Pro	Thr 635	Asp	Val	Ser	Cys	Glu 640
Gly	Leu	Gly	Ala	Trp 645	Val	Pro	Thr	Ala	Pro 650	Cys	Ala	Arg	Ile	Trp 655	Asn
Gly	Thr	Gln	Arg 660	Ala	Cys	Thr	Phe	Trp 665	Ala	Val	Asn	Ala	Tyr 670	Ser	Ser
Gly	Gly	Tyr 675	Ala	Gln	Leu	Ala	Ser	Tyr 680	Phe	Asn	Pro	Gly 685	Gly	Ser	Tyr
Tyr 690	Lys	Gln	Tyr	His	Pro	Thr 695	Ala	Cys	Glu	Val	Glu 700	Pro	Ala	Phe	Gly
His 705	Ser	Asp	Ala	Ala	Cys 710	Trp	Gly	Phe	Pro	Thr 715	Asp	Thr	Val	Met	Ser 720
Val	Phe	Ala	Leu	Ala	Ser	Tyr	Val	Gln	His 730	Pro	His	Lys	Thr	Val	Arg 735

Val	Lys	Phe	His	Thr	Glu	Thr	Arg	Thr	Val	Trp	Gln	Leu	Ser	Val	Ala	
			740					745					750			
Gly	Val	Ser	Cys	Asn	Val	Thr	Thr	Glu	His	Pro	Phe	Cys	Asn	Thr	Pro	
		755					760					765				
His	Gly	Gln	Leu	Glu	Val	Gln	Val	Pro	Pro	Asp	Pro	Gly	Asp	Leu	Val	
	770					775					780					
Glu	Tyr	Ile	Met	Asn	Tyr	Thr	Gly	Asn	Gln	Gln	Ser	Arg	Trp	Gly	Leu	
785					790					795					800	
Gly	Ser	Pro	Asn	Cys	His	Gly	Pro	Asp	Trp	Ala	Ser	Pro	Val	Cys	Gln	
			805					810						815		
Arg	His	Ser	Pro	Asp	Cys	Ser	Arg	Leu	Val	Gly	Ala	Thr	Pro	Glu	Arg	
			820					825					830			
Pro	Arg	Leu	Arg	Leu	Val	Asp	Ala	Asp	Asp	Pro	Leu	Leu	Arg	Thr	Ala	
		835				840						845				
Pro	Gly	Pro	Gly	Glu	Val	Trp	Val	Thr	Pro	Val	Ile	Gly	Ser	Gln	Ala	
	850					855					860					
Arg	Lys	Cys	Gly	Leu	His	Ile	Arg	Ala	Gly	Pro	Tyr	Gly	His	Ala	Thr	
865					870					875					880	
Val	Glu	Met	Pro	Glu	Trp	Ile	His	Ala	His	Thr	Thr	Ser	Asp	Pro	Trp	
				885					890					895		
His	Pro	Pro	Gly	Pro	Leu	Gly	Leu	Lys	Phe	Lys	Thr	Val	Arg	Pro	Val	
			900					905					910			
Ala	Leu	Pro	Arg	Ala	Leu	Ala	Pro	Pro	Arg	Asn	Val	Arg	Val	Thr	Gly	
		915					920					925				
Cys	Tyr	Gln	Cys	Gly	Thr	Pro	Ala	Leu	Val	Glu	Gly	Leu	Ala	Pro	Gly	
	930					935					940					
Gly	Gly	Asn	Cys	His	Leu	Thr	Val	Asn	Gly	Glu	Asp	Val	Gly	Ala	Phe	
945					950					955					960	
Pro	Pro	Gly	Lys	Phe	Val	Thr	Ala	Ala	Leu	Leu	Asn	Thr	Pro	Pro	Pro	
				965					970				975			
Tyr	Gln	Val	Ser	Cys	Gly	Gly	Glu	Ser	Asp	Arg	Ala	Ser	Ala	Gly	His	
			980					985					990			

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro	Ser	Arg	Ala	Pro	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Arg	Met	Gln	Thr
1				5				10						15	